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The Annexins

March 20th-24th, 2005

Monte Verità, Ascona

Annette Draeger, Bern

Stephen Moss, London

Volker Gerke, Münster

INTEGRATING EVOLUTIONARY AND EXPERIMENTAL MODELS OF ANNEXIN GENE EXPRESSION AND PROTEIN FUNCTION.

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Studies of gene family evolution use comparative genomics and proteomics along with phylogenetic and other computational analyses to reconstruct the speciation history and characterize the structure-function relationships among homologous members. The conservation and change of various features such as locus number, gene structures or protein domains provide objective, independent insight into what may represent significant components of annexin function, either universal or adaptive. The burgeoning wealth of sequence, structural and expression data on annexins and the plethora of bioinformatic tools have enabled us to revise, devise and demise concepts about how annexins may function. While this adds to the known multiplicity of properties and actions of annexins, it also contributes theoretical perspective and statistical validation that can be useful to predict and evaluate experimental data. The utility of hidden Markov models, sequence logos, 3D-models and phylogenetic footprinting for incorporating evolutionary information will be demonstrated with examples. To the extent that theoretical analyses, directed empirical research within the field, and collateral encounters (of the third kind) outside the field all contribute relevant information, it behooves us to examine the extent to which these knowledge domains are mutually compatible and whether the consolidated results can help direct our research to some viable definition of annexin function. The differentiation between intrinsic function and derived properties will be confronted from an evolutionary perspective. Other novel, controversial and dogmatic topics to be treated include the mechanisms and specificity of annexin membrane binding, putative ligand-receptor interactions, the importance of expression and localization, the ion channel hypothesis, and identifiable associations between structure and function, genotype and phenotype. Debate will be provocative and prizes will be awarded.